MARKED-UP VERSION OF AMENDED PARAGRAPHS IN THE SPECIFICATION

In the following amendments, underlining denotes added text while bracketing denotes deleted text. For the Tables, the only changes involve deleting the original shading within some cells and replacing it with text boxes. As these changes are too difficult to show with underlining and bracketing, no underlining or bracketing are used below. Should the Examiner require a different format to indicate these amendments, she is encouraged to contact Applicants.

IN THE SPECIFICATION:

Please replace the paragraph on page 1 under "Cross-Reference to Related Applications" with the following:

Pursuant to 35 U.S.C. §119(e), the present application claims benefit of and priority to US Application No. 60/233,610, entitled "Twin-Arginine Translocation in Bacillus", filed September 18, 2000[1] by Jongbloed et al.

Please replace Table I and the text following the Table, on page 56 with the following:

Table I. Predicted Twin-Arginine Signal Peptides of *B. subtilis

protein	signal peptide
AlbB	SPAQRRILLYILSFIFVIGAVVYFVKSDYLFTLIFIAIAILF
AmyX™	MVSIRRSFEAYVDDMNIITVLIPAEQKEIM
AppB™	MAAYIIRRTLMSIPILLGITILSFVIMKAAPG
LipA	MKFVKRRIIALVTILMLSVTSLFALQPSAKAAEH
OppB™	MLKYIGRRLVYMIITLFVIVTVTFFLMQAAPG
PbpX	MTSPTRRRTAKRRRRKLNKRGKLLFGLLAVMVCITIWNALHR
PhoD	MAYDSRFDEWVQKLKEESFQNNTFDRRKFIQGAGKIAGLSLGLTIAQSVGAFEV
QcrA	MGGKHDISRRQFLNYTLTGVGGFMAASMLMPMVRFA
SpoIIIJ™	MLLKRRIGLLLSMVGVFMLLAGCSSV
TlpA™	MKKTLTTIRRSSIARRLIISFLLILIVPITALSVSAYQS
WapA	MKKRKRRNFKRFIAAFLVLALMISLVPADVLAKST
WprA	KRRKFSSVVAAVLIFALIFSLFSPGTKAAAAGA
YceA™	MEMFDLEFMRRAFLAGGMIAVMAPILGVYLVLRRQ
YdeJ	MKKRRKICYCNTALLLMILLAGCTDS
YdhF	*MRRILSILVFAIMLAGCSSN*
YdhK	MSAGKSYRKKMKQRRMNMKISKYALGILMLSLVFVLSACGNNN
YesM™	KKRVAGWYRRMKIKDKLFVFLSLIMAVSFLFVYSGVQYAFHV
YesW	MRRSCLMIRRRKRMFTAVTLLVLLVMGTSVCPVKAEGA
YfkN™	MRIQKRRTHVENILRILLPPIMILSLILPTPPIHAEES
YkpC	MLRDLGRRVAIAAILSGIILGGMSISLANMP
YkuE	MKKMSRRQFLKGMFGALAAGALTAGGGYGYARYL
YmaC	MRRFLLNVILVLAIVLFLRYVHYSLEPE
YmzC	MFESEAELRRIRIALVWIAVFLLFGACGN
YubF™	MQKYRRRNTVAFTVLAYFTFFAGVFLFSIGLYNADNL
YuiC	MMLNMIRRLLMTCLFLLAFGTTFLSVSGIEAKDL
YvhJ	MAERVRVRVRKKKKSKRRKILKRIMLLFALALLVVVGLGGYKLY
YwbN	MSDEQKKPEQIHRRDILKWGAMAGAAVAIGASGLGGLAPLVQTAAKP

* Putative twin-arginine signal peptides were identified in two ways. First, the presence of the

consensus sequence R-R-X-ϕ-ϕ (ϕ is a hydrophobic residue), immediately in front of an amino-terminal hydrophobic region as predicted with the TopPred2 algorithm (34, 35), was determined. To this purpose, the first 60 residues of all annotated proteins of *B. subtilis* in the SubtiList database (http://bioweb.pasteur.fr/Genolist/Subtilist.html) were used. Second, within the group of twin-arginine membrane sorting signals, cleavable signal peptides were identified with the SignalP algorithm (61, 62). Conserved residues of the twin-arginine consensus sequence (R-R-X-ϕ-ϕ) are indicated in bold. In addition, positively charged residues that could function as a so-called Sec-avoidance signal (54) are indicated in bold and italics. The hydrophobic H-domain is indicated ~~in gray shading~~ in boxed text. In signal peptides with a predicted signal peptidase I cleavage site, residues from position –3 to –1 relative to the signal peptidase I cleavage site are underlined. Notably, some of these proteins contain one or more putative transmembrane segments elsewhere in the protein (indicated with "TM"), or are putative lipoproteins. Residues forming a so-called lipobox for signal peptidase II cleavage are enlarged in size.

Please replace Table IV and following text, on page 59, with the following:

Table IV. Twin-Arginine Signal Peptides of PhoD and PhoD-like proteins*

protein	signal peptide
PhoD (Bsu)	MAYDSRFDEWVQKLKEESFQNNTFD**RRK*FI***QGAGKIAGLSLGLTIAQSVGAFEV
SP1 (Sco)	MTPANHQAPTSAPSPAPSQSSHAPELRAAARSLG**RRRFLT**VTGAAAALAFAVNLPAAGTA SAAEL
SP2 (Sco)	MAPTGRPSALAEHAFSPHDAVLGAAARHLG**RRRFLT**VTAAAAALAFSTNLPARGAVAAPE
SP3 (Sco)	MTSRHRASENSRTPS**RRTVVK**AAAAGAVLAAPLAAALPAGAADAAPA
SP4 (Ste)	MTPAARPSQHAPELRAAARHLG**RRRFLT**VTGAAAALAFAVNLPAAGTAAAAEL

* Homologues of *B. subtilis* PhoD were identified by amino acid sequence similarity searches in GenBank using the BLAST algorithm. SP1 (Sco), gene SCC75A.32c of *Streptomyces coelicolor* (CAB61732); SP2 (Sco), gene SCF43A.18 of *S. coelicolor* (CAB48905); SP3 (Sco), gene SC4G6.37 of *S. coelicolor* (CAB51460), and SP4, *phoD* gene of *Streptomyces tendae*

(CAB62565). GenBank accession numbers are indicated in parentheses. Conserved residues of the twin-arginine consensus sequence are indicated in bold. The hydrophobic H-region is indicated by boxed text. ~~in in gray shading.~~ Signal peptidase I recognition sequences predicted with the SignalP algorithm (61, 62) are underlined.